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## SEQUENCE LISTING

<110> MARINE BIOTECHNOLOGY INSTITUTE CO., LTD.

<120> A NOVEL CAROTENOID HYDROXYLASE GENE AND A METHOD FOR PRODUCING HYDROXY CAROTENOID AND A NOVEL GERANYLGERANYLPYROPHOSPHATE SYNTHETASE GENE

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<150> JP 2003/388165

<151> 2003-11-26

<150> JP 2004/165919

<151> 2004-06-03

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175 180 185 190	
tgg ccc gcc gcc tgg ctg gag cgg gcg ccg ctt cgc tgg ctg atc acc	11365
Trp Pro Ala Ala Trp Leu Glu Arg Ala Pro Leu Arg Trp Leu Ile Thr	
195 200 205	
gcc acc cac cac gac gcc cac cac aag cgg ttc aac gga aac tac ggc	11413
Ala Thr His His Asp Ala His His Lys Arg Phe Asn Gly Asn Tyr Gly	
210 215 220	
ctc tat ttc cag ttc tgg gac cgc tgg gcc ggg act gag gtt tcg gcc	11461
Leu Tyr Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala	
225 230 235	
gcc ccc tcg cca cca tcc ccg gtc atc cct cca gag cgg ccc tca gcg	11509
Ala Pro Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala	
240 245 250	
cct ctt cgg tcatcggttt ggtcaggcg ggcgtggcg cccaggccgg	11558
Pro Leu Arg	
255	
tcggccatctg cagttatggac gacgaggcca gacgtcccccc gccgctcatg gcgatgaccc	11618
gcaggaggatc cctcaaatgc cgggtgtcca tcatgaagtt cagcccgatcg cggtccggca	11678
tcagaatgtc caccagcact gcgtcggcg accagtccctc gacgatccgc aaccgcgtgt	11738
tgaccgttgc tgcggtcagg acttggcaac ccagccgttt cagcatctcc tccagatgaa	11798

gcagaaccag cgaatcgcc tcgatcacgc agactttcac gcccaacctc cagatgcgat	11858
cagggggAAC taacggatga atcccatgtt gcgtcaactc ggaagacggc gtttccgact	11918
ggccatcgcc ttggcgggcg cggcgtgac cctgcttctg gcggccactg gggtgacgct	11978
gcaacgagaa ttc	11991

<210> 3  
 <211> 774  
 <212> DNA  
 <213> Brevundimonas sp.

<220>  
 <221> CDS  
 <222> (1).. (771)

<400> 3				
atg ttg agg gat ctg ctc atc acc acc ctg gcg ctg agc ctg atc atc	48			
Met Leu Arg Asp Leu Leu Ile Thr Thr Leu Ala Leu Ser Leu Ile Ile				
1 5 10 15				
ggc ctg cgc tat ctg ctg gtc ggc gcg gcc cat ggg ctg ctg tgg	96			
Gly Leu Arg Tyr Leu Leu Val Gly Ala Ala Ala His Gly Leu Leu Trp				
20 25 30				
gcc ggg gcg ggc cgg gga cgg gcg ctg aac ctg cgg ccg ccg gcg atg	144			
Ala Gly Ala Gly Arg Gly Arg Ala Leu Asn Leu Arg Pro Pro Ala Met				
35 40 45				
aag cgc atc cgc gcc gag atc gtc gcc tcc ctg atc gcc tgc ccc atc	192			
Lys Arg Ile Arg Ala Glu Ile Val Ala Ser Leu Ile Ala Cys Pro Ile				
50 55 60				
tac gcc ctg ccg gcg gcc ctg gtg ctg gag ctg tgg aag cgg ggc ggg	240			
Tyr Ala Leu Pro Ala Ala Leu Val Leu Glu Leu Trp Lys Arg Gly Gly				
65 70 75 80				
acg gcg atc tac agc gat ccc gac gcc tgg ccc ctg tgg tgg ctg ccg	288			
Thr Ala Ile Tyr Ser Asp Pro Asp Ala Trp Pro Leu Trp Trp Leu Pro				
85 90 95				
gtc agt ctg atc gtc tat ctg ctg gcg cac gac gcc ttc tac tac tgg	336			
Val Ser Leu Ile Val Tyr Leu Leu Ala His Asp Ala Phe Tyr Tyr Trp				
100 105 110				

gtg cac agg gcc ctg cat cac ccg cgc gtc ttc ggc tgg gcc cat gcc	384		
Val His Arg Ala Leu His His Pro Arg Val Phe Gly Trp Ala His Ala			
115	120	125	
gaa cac cac cgg tcg cgc gac ccc agc gcc ttc gcc tcc ttc gcc ttc	432		
Glu His His Arg Ser Arg Asp Pro Ser Ala Phe Ala Ser Phe Ala Phe			
130	135	140	
gac ccg gcc gag gct gcg gcc acc gcc tgg ttc ctg ccc gcc ctg gcc	480		
Asp Pro Ala Glu Ala Ala Ala Thr Ala Trp Phe Leu Pro Ala Leu Ala			
145	150	155	160
ctg atc gtg ccg atc cac tgg ggc gtg gcc ctg acc ctg ctg acg ctg	528		
Leu Ile Val Pro Ile His Trp Gly Val Ala Leu Thr Leu Leu Thr Leu			
165	170	175	
atg tcg ctg acg gcc ctg aac cat gcg ggg cgc gag gtc tgg ccc	576		
Met Ser Leu Thr Ala Ala Leu Asn His Ala Gly Arg Glu Val Trp Pro			
180	185	190	
gcc gcc tgg ctg gag cgg gcg ccc ttt cgc tgg ctg atc acc gcc acc	624		
Ala Ala Trp Leu Glu Arg Ala Pro Leu Arg Trp Leu Ile Thr Ala Thr			
195	200	205	
cac cac gac gcc cac cac aag cgg ttc aac gga aac tac ggc ctc tat	672		
His His Asp Ala His His Lys Arg Phe Asn Gly Asn Tyr Gly Leu Tyr			
210	215	220	
ttc cag ttc tgg gac cgc tgg gcc ggg act gag gtt tcg gcc gcc ccc	720		
Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala Ala Pro			
225	230	235	240
tcg cca cca tcc ccg gtc atc cct cca gag cgg ccc tca gcg cct ctt	768		
Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala Pro Leu			
245	250	255	
cggtga	774		
Arg			

<210> 4  
 <211> 257  
 <212> PRT  
 <213> Brevundimonas sp.

<400> 4  
 Met Leu Arg Asp Leu Leu Ile Thr Thr Leu Ala Leu Ser Leu Ile Ile  
 1 5 10 15

Gly Leu Arg Tyr Leu Leu Val Gly Ala Ala Ala His Gly Leu Leu Trp  
 20 25 30

Ala Gly Ala Gly Arg Gly Arg Ala Leu Asn Leu Arg Pro Pro Ala Met  
 35 40 45

Lys Arg Ile Arg Ala Glu Ile Val Ala Ser Leu Ile Ala Cys Pro Ile  
 50 55 60

Tyr Ala Leu Pro Ala Ala Leu Val Leu Glu Leu Trp Lys Arg Gly Gly  
 65 70 75 80

Thr Ala Ile Tyr Ser Asp Pro Asp Ala Trp Pro Leu Trp Trp Leu Pro  
 85 90 95

Val Ser Leu Ile Val Tyr Leu Leu Ala His Asp Ala Phe Tyr Tyr Trp  
 100 105 110

Val His Arg Ala Leu His His Pro Arg Val Phe Gly Trp Ala His Ala  
 115 120 125

Glu His His Arg Ser Arg Asp Pro Ser Ala Phe Ala Ser Phe Ala Phe  
 130 135 140

Asp Pro Ala Glu Ala Ala Ala Thr Ala Trp Phe Leu Pro Ala Leu Ala  
 145 150 155 160

Leu Ile Val Pro Ile His Trp Gly Val Ala Leu Thr Leu Leu Thr Leu  
 165 170 175

Met Ser Leu Thr Ala Ala Leu Asn His Ala Gly Arg Glu Val Trp Pro  
 180 185 190

Ala Ala Trp Leu Glu Arg Ala Pro Leu Arg Trp Leu Ile Thr Ala Thr  
 195 200 205

His His Asp Ala His His Lys Arg Phe Asn Gly Asn Tyr Gly Leu Tyr  
 210 215 220

Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala Ala Pro  
 225 230 235 240

Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala Pro Leu  
 245 250 255

Arg

<210> 5  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 5  
tacgaattcg atgcccctcg ccctg 25

<210> 6  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 6  
tagaggatcc tcaaggatgc aactggatcg ta 32

<210> 7  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 7  
tacgaattcg atgaccggccg ccgtcg 26

<210> 8  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 8

tagaggatcc tcaagactcg ccgcgccaca a

31

<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 9  
tacgaattcg ctgtcgcgga tgcaggc

27

<210> 10  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 10  
tagaggatcc tgcggttcag cagccgataa aa

32

<210> 11  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 11  
tacgaattcg atgcgagcag cagtgtatcg a

31

<210> 12  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 12

tagaggatcc aagctcttgg agccctgct 29

<210> 13  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 13  
tacgaattcg atgagcgcacg ccgtcct 27

<210> 14  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 14  
tagaggatcc tcagatgtgg gtccacagg 29

<210> 15  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 15  
tacgaattcg atgatggcgg tggcggc 28

<210> 16  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 16

tagaggatcc cccacatctg acggcgct

28

<210> 17  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 17  
tacgaattcg atgtccttca tctcttccgg c

31

<210> 18  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 18  
tagaggatcc accgccatca tgacgagg

28

<210> 19  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 19  
tacgaattcg atggcgatcg tcggctaa

29

<210> 20  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 20

tagaggatcc ctagcgtcca agttcggcct 30

<210> 21  
<211> 29  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:primer

<400> 21  
tacgaattcg atgcccaccc ccgacgacg 29

<210> 22  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 22  
tagaggatcc tcagaagcgg ggctcttcca 30

<210> 23  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 23  
tacgaattcg atggcctggc tgacgtggat 30

<210> 24  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 24

tagaggatcc tcaggcgccg ctgctggaa 29

<210> 25  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 25  
tacgaattcg atgttggagg atctgctcat ca 32

<210> 26  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 26  
tagaggatcc tcaccgaaga ggcgcgtgag 29

<210> 27  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 27  
tacgaattcg atgctgaaac ggctgggtt 29

<210> 28  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 28

tagaggatcc ctatccat ttcggacc g 31  
 <210> 29  
 <211> 486  
 <212> DNA  
 <213> Brevundimonas sp.  
 <220>  
 <221> CDS  
 <222> (1).. (483)  
 <400> 1  
 atg gcc tgg ctg acg tgg atc gcg ctg ttc ctg acc gcc ttt ttg ggc 48  
 Met Ala Trp Leu Thr Trp Ile Ala Leu Phe Leu Thr Ala Phe Leu Gly  
 1 5 10 15  
 atg gag gcg ttc gcc tgg atc atg cac cgc tat gtg atg cac gac ggt ttc 96  
 Met Glu Ala Phe Ala Trp Ile Met His Arg Tyr Val Met His Gly Phe  
 20 25 30  
 ctg tgg tcc tgg cac cgc agc cat cat gag ccc cac gat cac ccc ctg 144  
 Leu Trp Ser Trp His Arg Ser His His Glu Pro His Asp His Pro Leu  
 35 40 45  
 gag aag aac gac ctg ttc gcc gtg gtc ttc gcc ccc gac atc gtc 192  
 Glu Lys Asn Asp Leu Phe Ala Val Val Phe Ala Ala Pro Ala Ile Val  
 50 55 60  
 atg gtg gcc gtg ggt ctg cac ctg tgg ccc tgg gcc ctg ccc gtc ggc 240  
 Met Val Ala Val Gly Leu His Leu Trp Pro Trp Ala Leu Pro Val Gly  
 65 70 75 80  
 ctg ggg atc acg gcc tat ggg atg gtc tat ttc ttc cac gac ggc 288  
 Leu Gly Ile Thr Ala Tyr Gly Met Val Tyr Phe Phe His Asp Gly  
 85 90 95  
 ctg gtg cac cgg cgg ttc ccg acg ggc ttt tcc ggg cgg tcc ggc ttc 336  
 Leu Val His Arg Arg Phe Pro Thr Gly Phe Ser Gly Arg Ser Gly Phe  
 100 105 110  
 tgg acg cgg cgc atc cag gcg cac cgt ctg cat cac gcc gtg cgc acg 384  
 Trp Thr Arg Arg Ile Gln Ala His Arg Leu His His Ala Val Arg Thr  
 115 120 125  
 cgc gaa ggc tgc gtc tcc ttc ggc ttt ctg tgg gtg cgg tcg gcg cgg 432  
 Arg Glu Gly Cys Val Ser Phe Gly Phe Leu Trp Val Arg Ser Ala Arg  
 130 135 140

gct ctg aag gcc gaa ctg gct cag cgg ggc tct tcc agc agc ggc 480  
 Ala Leu Lys Ala Glu Leu Ala Gln Lys Arg Gly Ser Ser Ser Gly  
 145 150 155 160

gcc tga 486  
 Ala

<210> 30  
 <211> 161  
 <212> PRT  
 <213> Brevundimonas sp.

<400> 30  
 Met Ala Trp Leu Thr Trp Ile Ala Leu Phe Leu Thr Ala Phe Leu Gly  
 1 5 10 15

Met Glu Ala Phe Ala Trp Ile Met His Arg Tyr Val Met His Gly Phe  
 20 25 30

Leu Trp Ser Trp His Arg Ser His His Glu Pro His Asp His Pro Leu  
 35 40 45

Glu Lys Asn Asp Leu Phe Ala Val Val Phe Ala Ala Pro Ala Ile Val  
 50 55 60

Met Val Ala Val Gly Leu His Leu Trp Pro Trp Ala Leu Pro Val Gly  
 65 70 75 80

Leu Gly Ile Thr Ala Tyr Gly Met Val Tyr Phe Phe Phe His Asp Gly  
 85 90 95

Leu Val His Arg Arg Phe Pro Thr Gly Phe Ser Gly Arg Ser Gly Phe  
 100 105 110

Trp Thr Arg Arg Ile Gln Ala His Arg Leu His His Ala Val Arg Thr  
 115 120 125

Arg Glu Gly Cys Val Ser Phe Gly Phe Leu Trp Val Arg Ser Ala Arg  
 130 135 140

Ala Leu Lys Ala Glu Leu Ala Gln Lys Arg Gly Ser Ser Ser Gly  
 145 150 155 160

Ala

<210> 31  
<211> 897  
<212> DNA  
<213> *Brevundimonas* sp.

<220>  
<221> CDS  
<222> (1).. (894)

<400> 31  
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 Met Ala Ile Val Gly Leu Arg Pro Gln Pro Val Ser Asp Pro Glu Pro  
 1 . 5 10 15  
 cag tcg ccc gag aat ctg cgt ggc ctg gtg cag gac cgg ctg gcc gag  
 Gln Ser Pro Glu Asn Leu Arg Gly Leu Val Gln Asp Arg Leu Ala Glu  
 20 25 30 96  
 acg gcg ccc tca tcg gac ggt ctt tta gcc ctc gcc gcg cgc gag gcc  
 Thr Ala Pro Ser Ser Asp Gly Leu Leu Ala Leu Ala Ala Arg Glu Ala  
 35 40 45 144  
 ctg ctg gga ccg ggc aag cgg gtc agg ccg gtc gtg gcc atg ttg gcc  
 Leu Leu Gly Pro Gly Lys Arg Val Arg Pro Val Val Ala Met Leu Ala  
 50 55 60 192  
 gcc gcg cac gtc ggc ggg cgg gcc gag gac gcc ctg gat ttc ggt tgc  
 Ala Ala His Val Gly Gly Arg Ala Glu Asp Ala Leu Asp Phe Gly Cys  
 65 70 75 80 240  
 gcg gtc gaa atg gcc cat gcc tcc ctg gtt ctg gac gac ctg ccc  
 Ala Val Glu Met Ala His Ala Ala Ser Leu Val Leu Asp Asp Leu Pro  
 85 90 95 288  
 tgt atg gat gat gcg gcc ttg cgg cgc ggt cag ccg acc ctg cac cgc  
 Cys Met Asp Asp Ala Ala Leu Arg Arg Gly Gln Pro Thr Leu His Arg  
 100 105 110 336  
 cgc cac ggc gag gat gcg gcc gtg ctg gcg gcc gtg gcc ctt ttg aac  
 Arg His Gly Glu Asp Ala Ala Val Leu Ala Ala Val Ala Leu Leu Asn  
 115 120 125 384  
 caa tcg acc cgg ctg att ctg caa agc cgg gcg ccg tcg gag gcg cgg  
 Gln Ser Thr Arg Leu Ile Leu Gln Ser Arg Ala Pro Ser Glu Ala Arg  
 130 135 140 432  
 ctg ggc gcc ctg gac gat ttg acg cag gcg atc ggc ttc gac ggc ctg  
 480

Leu	Gly	Ala	Leu	Asp	Asp	Leu	Thr	Gln	Ala	Ile	Gly	Phe	Asp	Gly	Leu
145						150					155				160
gcc gag ggc cag atg cgc gat ctg cgc gac gat ccc gtt cag cgc gac															528
Ala	Glu	Gly	Gln	Met	Arg	Asp	Leu	Arg	Asp	Asp	Pro	Val	Gln	Arg	Asp
						165					170				175
gtg gtc gcc ctg cgt cgg atc aac gat ctg aag acc ggc gcc ctg ttc															576
Val	Val	Ala	Leu	Arg	Arg	Ile	Asn	Asp	Leu	Lys	Thr	Gly	Ala	Leu	Phe
						180					185				190
gtc gcg gcc gcg cgg ggc ggc ggc cgg atg ggc ggc ggc gat gcg gac															624
Val	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Met	Gly	Gly	Gly	Asp	Ala	Asp	
						195					200				205
gac ctg gcg cgt ctc gcc gcc ttc ggc gaa gcg gtc ggc ttc gcc ttc															672
Asp	Leu	Ala	Arg	Leu	Ala	Ala	Phe	Gly	Glu	Ala	Val	Gly	Phe	Ala	Phe
						210					215				220
cag ctt tgc gac gac ctg atg gac gcc tgt tcg acg agc gag gcc ttg															720
Gln	Leu	Cys	Asp	Asp	Leu	Met	Asp	Ala	Cys	Ser	Thr	Ser	Glu	Ala	Leu
						225					230				235
ggc aag gac gtg ggt cag gat cag ggc gtg acc acc ttc gtg gac ctg															768
Gly	Lys	Asp	Val	Gly	Gln	Asp	Gln	Gly	Val	Thr	Thr	Phe	Val	Asp	Leu
						245					250				255
tgg ggc gaa ggc cgg gtc cgc gcc ggg gtg cgc cag tca ctg gcc cgg															816
Trp	Gly	Glu	Gly	Arg	Val	Arg	Ala	Gly	Val	Arg	Gln	Ser	Leu	Ala	Arg
						260					265				270
gcg gcc gag gcg gtc ggg cac gac agc ccc ctg acg acc tat gtc ctt															864
Ala	Ala	Glu	Ala	Val	Gly	His	Asp	Ser	Pro	Leu	Thr	Thr	Tyr	Val	Leu
						275					280				285
cat ctc ttc cgg cag gcc gaa ctt gga cgc tag															897
His	Leu	Phe	Arg	Gln	Ala	Glu	Leu	Gly	Arg						
						290					295				
<210> 32															
<211> 298															
<212> PRT															
<213> Brevundimonas sp.															
<400> 32															
Met	Ala	Ile	Val	Gly	Leu	Arg	Pro	Gln	Pro	Val	Ser	Asp	Pro	Glu	Pro
1			5							10					15

Gln Ser Pro Glu Asn Leu Arg Gly Leu Val Gln Asp Arg Leu Ala Glu  
 20 25 30

Thr Ala Pro Ser Ser Asp Gly Leu Leu Ala Leu Ala Ala Arg Glu Ala  
 35 40 45

Leu Leu Gly Pro Gly Lys Arg Val Arg Pro Val Val Ala Met Leu Ala  
 50 55 60

Ala Ala His Val Gly Gly Arg Ala Glu Asp Ala Leu Asp Phe Gly Cys  
 65 70 75 80

Ala Val Glu Met Ala His Ala Ala Ser Leu Val Leu Asp Asp Leu Pro  
 85 90 95

Cys Met Asp Asp Ala Ala Leu Arg Arg Gly Gln Pro Thr Leu His Arg  
 100 105 110

Arg His Gly Glu Asp Ala Ala Val Leu Ala Ala Val Ala Leu Leu Asn  
 115 120 125

Gln Ser Thr Arg Leu Ile Leu Gln Ser Arg Ala Pro Ser Glu Ala Arg  
 130 135 140

Leu Gly Ala Leu Asp Asp Leu Thr Gln Ala Ile Gly Phe Asp Gly Leu  
 145 150 155 160

Ala Glu Gly Gln Met Arg Asp Leu Arg Asp Asp Pro Val Gln Arg Asp  
 165 170 175

Val Val Ala Leu Arg Arg Ile Asn Asp Leu Lys Thr Gly Ala Leu Phe  
 180 185 190

Val Ala Ala Ala Arg Gly Gly Arg Met Gly Gly Asp Ala Asp  
 195 200 205

Asp Leu Ala Arg Leu Ala Ala Phe Gly Glu Ala Val Gly Phe Ala Phe  
 210 215 220

Gln Leu Cys Asp Asp Leu Met Asp Ala Cys Ser Thr Ser Glu Ala Leu  
 225 230 235 240

Gly Lys Asp Val Gly Gln Asp Gln Gly Val Thr Thr Phe Val Asp Leu  
 245 250 255

Trp Gly Glu Gly Arg Val Arg Ala Gly Val Arg Gln Ser Leu Ala Arg  
 260 265 270

Ala Ala Glu Ala Val Gly His Asp Ser Pro Leu Thr Thr Tyr Val Leu  
275 280 285

His Leu Phe Arg Gln Ala Glu Leu Gly Arg  
290 295